

FIGURE 1

1
ATGGCTCCCTTAGCCGAAGTCGGGGGCTTTCTGGGCGGCCTGGAG
MetAlaProLeuAlaGluValGlyGlyPheLeuGlyGlyLeuGlu
46
GGCTTGGGCCAGCAGGTGGGTTCGCATTTCTGTTGCCTCCTGCC
GlyLeuGlyGlnGlnValGlySerHisPheLeuLeuProProAla
91
GGGAGCGGCCCGCTGCTGGGCGAGCGCAGGAGCGCGCGGAG
GlyGluArgProProLeuLeuGlyGluArgArgSerAlaAlaGlu
136
CGGAGCGCGCGCGGGCGGGGCTGCGCAGCTGGCGCACCTG
ArgSerAlaArgGlyGlyProGlyAlaAlaGlnLeuAlaHisLeu
181
CACGGCATCCTGCGCCGCCGGCAGCTCTATTGCCGCACCGGCTTC
HisGlyIleLeuArgArgArgGlnLeuTyrCysArgThrGlyPhe
226
CACCTGCAGATCCTGCCCCGACGGCAGCGTGCAGGGCACCCGGCAG
HisLeuGlnIleLeuProAspGlySerValGlnGlyThrArgGln
271
GACCACAGCCTCTTCGGTATCTTGAATTCATCAGTGTGGCAGTG
AspHisSerLeuPheGlyIleLeuGluPheIleSerValAlaVal
316
GGA CTGGTCAGTATTAGAGGTGTGGACAGTGGTCTCTATCTTGA
GlyLeuValSerIleArgGlyValAspSerGlyLeuTyrLeuGly
361
ATGAATGACAAAGGAGAACTCTATGGATCAGAGAACTTACTTCC
MetAsnAspLysGlyGluLeuTyrGlySerGluLysLeuThrSer
406
GAATGCATCTTTAGGGAGCAGTTTGAAGAGAACTGGTATAACACC
GluCysIlePheArgGluGlnPheGluGluAsnTrpTyrAsnThr
451
TATTCATCTAACATATATAAACATGGAGACACTGGCCGCAGGTAT
TyrSerSerAsnIleTyrLysHisGlyAspThrGlyArgArgTyr
496
TTTGTGGCACTTAACAAAGACGGA ACTCCAAGAGATGGCGCCAGG
PheValAlaLeuAsnLysAspGlyThrProArgAspGlyAlaArg
541
TCCAAGAGGCATCAGAAAATTTACACATTTCTTACCTAGACCAGTG
SerLysArgHisGlnLysPheThrHisPheLeuProArgProVal
586
GATCCAGAAAGAGTTCCAGAATTGTACAAGGACCTACTGATGTAC
AspProGluArgValProGluLeuTyrLysAspLeuLeuMetTyr
631
ACT
Thr

FIGURE 2

Query: 170 TGGCGCACCTGCACGGCATCCTGCGCCGCCGGCAGCTCTATTGCCGCACCGGCTTCCACC 229
 ||| || | | | | | | | | | | | | | | | | | | | | | |
 Sbjct: 2 TGGATCATTTAAAGGGGATTCTCAGGCGGAGGCAGCTATACTGCAGGACTGGATTTCAC 61

Query: 230 TGCAGATCCTGCCCCACGGCAGCGTGCAGGGCACCCGGCAGGACCACAGCCTCTTCGGTA 289
 | | | | | | | | | | | | | | | | | | | | | | | | | |
 Sbjct: 62 TAGAAATCTTCCCCAATGGTACTATCCAGGGAACCAGGAAAGACCACAGCCGATTTGGCA 121

Query: 290 TCTTGGAATTCATCAGTGTGGCAGTGGGACTGGTCAGTATTAGAGGTGTGGACAGTGGTC 349
 | | | | | | | | | | | | | | | | | | | | | | | | | |
 Sbjct: 122 TTCTGGAATTTATCAGTATAGCAGTGGGCCTGGTCAGCATTTCGAGGCGTGGACAGTGGAC 181

Query: 350 TCTATCTTGGAATGAATGACAAAGGAGAACTCTATGGATCAGAGAAACTTACTTCCGAAT 409
 ||| | | | | | | | | | | | | | | | | | | | | | | | |
 Sbjct: 182 TCTACCTCGGGATGAATGAGAAGGGGGAGCTGTATGGATCAGAAAACTAACCCAAGAGT 241

Query: 410 GCATCTTTAGGGAGCAGTTTGAAGAGAACTGGTATAACACCTATTCATCTAACATATATA 469
 | | | | | | | | | | | | | | | | | | | | | | | | | |
 Sbjct: 242 GTGTATTCAGAGAACAGTTTCGAAGAAAACCTGGTATAATACGTACTCGTCAAACCTATATA 301

Query: 470 AACATGGAGACACTGGCCGCAGGTATTTTGTGGCACTTAACAAAGACGGAACTCCAAGAG 529
 | | | | | | | | | | | | | | | | | | | | | | | | | |
 Sbjct: 302 AGCACGTGGACACTGGAAGGCGATACTATGTTGCATTAAATAAAGATGGGACCCCGAGAG 361

Query: 530 ATGGCGCCAGGTCCAAGAGGCATCAGAAATTTACACATTTCTTACCTAGACCAGTGGATC 589
 | | | | | | | | | | | | | | | | | | | | | | | | | |
 Sbjct: 362 AAGGGACTAGGACTAAACGGCACCAGAAATTCACACATTTTTTACCTAGACCAGTGGACC 421

Query: 590 CAGA 593
 | | |
 Sbjct: 422 CCGA 425

FIGURE 3

>gb:GenBank accession number -ID:AB020858|acc:AB020858 Homo sapiens genomic DNA of p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer , segment 1/11 - Homo sapiens, 100000 bp.

Minus Strand HSPs:

A.

Score = 1430 (214.6 bits), Expect = 1.6e-126, Sum P(3) = 1.6e-126
Identities = 288/289 (99%), Positives = 288/289 (99%),
Strand = Minus / Plus

```
Query:   289 TACCGAAGAGGCTGTGGTCCTGCCGGGTGCCCTGCACGCTGCCGTCGGGCAGGATCTGCA 230
          |||
Sbjct: 15927 TACCGAAGAGGCTGTGGTCCTGCCGGGTGCCCTGCACGCTGCCGTCGGGCAGGATCTGCA 15986

Query:   229 GGTGGAAGCCGGTGC GGCAATAGAGCTGCCGGCGGCGCAGGATGCCGTGCAGGTGCGCCA 170
          |||
Sbjct: 15987 GGTGGAAGCCGGTGC GGCAATAGAGCTGCCGGCG- CGCAGGATGCCGTGCAGGTGCGCCA 16045

Query:   169 GCTGCGCAGCCCCCGGCCCGCGCGCGCTCCGCTCCGCCGCGCTCCTGCGCTCGCCCA 110
          |||
Sbjct: 16046 GCTGCGCAGCCCCCGGCCCGCGCGCGCTCCGCTCCGCCGCGCTCCTGCGCTCGCCCA 16105

Query:   109 GCAGCGGCGGCGCTCCCCGGCAGGAGGCAACAGGAAATGCGAACCCACCTGCTGGCCCA 50
          |||
Sbjct: 16106 GCAGCGGCGGCGCTCCCCGGCAGGAGGCAACAGGAAATGCGAACCCACCTGCTGGCCCA 16165

Query:    49 AGCCCTCCAGGCCGCCCAGAAAGCCCCCGACTTCGGCTAAGGGAGCCAT 1
          |||
Sbjct: 16166 AGCCCTCCAGGCCGCCCAGAAAGCCCCCGACTTCGGCTAAGGGAGCCAT 16214
```

B.

Score = 1224 (183.6 bits), Expect = 1.6e-126, Sum P(3) = 1.6e-126
Identities = 250/255 (98%), Positives = 250/255 (98%),
Strand = Minus / Plus

```
Query:   633 AGTGATACATCAGTAGGTCCTTGTAACAATTCTGGAACCTCTTCTGGATCCACTGGTCTAGG 574
          |||
Sbjct: 7257 AGTGATACATCAGTAGGTCCTTGTAACAATTCTGGAACCTCTTCTGGATCCACTGGTCTAGG 7316

Query:   573 TAAGAAATGTGTAAATTTCTGATGCCTCTTGGACCTGGCGCCATCTCTTGAGTTCCGTC 514
          |||
Sbjct: 7317 TAAGAAATGTGTAAATTTCTGATGCCTCTTGGACCTGGCGCCATCTCTTGAGTTCCGTC 7376

Query:   513 TTTGTTAAGTGCCACAAAATACCTGCGGCCAGTGTCTCCATGTTTATATATGTTAGATGA 454
          |||
Sbjct: 7377 TTTGTTAAGTGCCACAAAATACCTGCGGCCAGTGTCTCCATGTTTATATATGTTAGATGA 7436

Query:   453 ATAGGTGTTATACCACTTCTCTTCAAAGTCTCCCTAAAGATGCATTCCGGAAGTAAGTTT 394
          |||
Sbjct: 7437 ATAGGTGTTATACCACTTCTCTTCAAAGTCTCCCTAAAGATGCATTCCGGAAGTAAGTTT 7496
```

C.

```

Query:      391 CTGATCCATAGAGTTCTCCTTTGTCAATTCATTCCAAGATAGAGACCACTGTCCACACCTC 332
             |||
Sbjct:     9837 CTGATCCATAGAGTTCTCCTTTGTCAATTCATTCCAAGATAGAGACCACTGTCCACACCTC 9896

Query:      331 TAATACTGACCAGTCCCACTGCCACACTGATGAATTCCAAGATACC 286
             |||
Sbjct:     9897 TAATACTGACCAGTCCCACTGCCACACTGATGAATTCCAAGATACC 9942

```

FIGURE 4

Sequences analyzed:

1. HUMAN FGF-9 (P31371_HUMAN FGF-9) [SEQ ID NO:9]
2. MOUSE FGF-9 (P54130_MOUSE FGF-9) [SEQ ID NO:10]
3. RAT FGF-9 (P36364_FGF9_RAT FGF-9) [SEQ ID NO:11]
4. XENOPUS XFGF-CX (BAA83474Xen; Xenopus laevis XFGF-CX) [SEQ ID NO:12]
5. FGF-CX (cgAB020858) [SEQ ID NO:2]

Multiple Alignment:

HUMAN FGF-9
RAT FGF-9
MOUSE FGF-9
XENOPUS XFGF-CX
FGF-CX

```

M A P L G E V G N Y F G V Q D A V P - - F G N V P V L P - - V D S P V L L S D H L G Q S E A G G L P R G P A V T D L D H
M A P L G E V G S Y F G V Q D A V P - - F G N V P V L P - - V D S P V L L S D H L G Q S E A G G L P R G P A V T D L D H
M A P L G E V G S Y F G V Q D A V P - - F G N V P V L P - - V D S P V L L S D H L G Q S E A G G L P R G P A V T D L D H
M A P L A D V G T E L G G Y D A T G - Q V G S H F F L L P P A K D S P L L F N D P L A Q S E R L S R - S T P - S D L S H
M A P L A E V G G F L G L E G L G Q Q V G S H F L L P P A G E R P P L L G R R S A A E R S A R - G G P C A A Q L L A H

```

HUMAN FGF-9
RAT FGF-9
MOUSE FGF-9
XENOPUS XFGF-CX
FGF-CX

```

L K G I L R R R Q L Y C R T G F H L E I F P N G T I Q G T R K D H S R F G I L E F I S I A V G L V S I R G V D S G L Y L
L K G I L R R R Q L Y C R T G F H L E I F P N G T I Q G T R K D H S R F G I L E F I S I A V G L V S I R G V D S G L Y L
L K G I L R R R Q L Y C R T G F H L E I F P N G T I Q G T R K D H S R F G I L E F I S I A V G L V S I R G V D S G L Y L
L Q G I L R R R Q L Y C R T G F H L Q I L P D G N V Q G T R Q D H S R F G I L E F I S I A V G L V S I R G V D S G L Y L
L H G I L R R R Q L Y C R T G F H L Q I L P D G S V Q G T R Q D H S R F G I L E F I S I A V G L V S I R G V D S G L Y L

```

HUMAN FGF-9
RAT FGF-9
MOUSE FGF-9
XENOPUS XFGF-CX
FGF-CX

```

G M N E K G E L Y G S E K L T Q E C V F R E Q F E E N W Y N T Y S S N L Y K H V D T G R R Y Y V A L N K D G T P R E G T
G M N E K G E L Y G S E K L T Q E C V F R E Q F E E N W Y N T Y S S N L Y K H V D T G R R Y Y V A L N K D G T P R E G T
G M N E K G E L Y G S E K L T Q E C V F R E Q F E E N W Y N T Y S S N L Y K H V D T G R R Y Y V A L N K D G T P R E G T
G M N E K G E L Y G S E K L T S E C I F R E Q F E E N W Y N T Y S S N L Y K H G D S G R R Y Y V A L N K D G T P R E G T
G M N E K G E L Y G S E K L T S E C I F R E Q F E E N W Y N T Y S S N L Y K H G D I T G R R Y Y V A L N K D G T P R E G T

```

HUMAN FGF-9
RAT FGF-9
MOUSE FGF-9
XENOPUS XFGF-CX
FGF-CX

```

R T K R H Q K F T H F L P R P V D P D K V P E L Y K D I L S Q S
R T K R H Q K F T H F L P R P V D P D K V P E L Y K D I L S Q S
R T K R H Q K F T H F L P R P V D P D K V P E L Y K D I L S Q S
R A K R H Q K F T H F L P R P V D P D K V P E L Y K D I L M G Y S
R S K R H Q K F T H F L P R P V D P D K V P E L Y K D I L M Y T

```

FIGURE 5

| | | | | | | | | |
|---------|---------------------|-----------------|-------------------------|---------------|----------------|------------|-------|-----|
| FGF-CX | MAPLAEVGGFL | EGLEGLGQ | QVSSHFLPPA | GERPPL | GERSSAERSAR | GGPAAQLAH | 59 | |
| XFGF-20 | MAPLAEVGTFL | GGYDALG | QVSSHFLPPA | KDSPL | FENDPLAQSEELSR | SAP--SDLSH | 56 | |
| FGF-9 | MAPLSEVGNV | FGVQDAWP | --FENVPLP-- | VDSFWLLSDHL | GQSEAGGLPREP | AVTDLDH | 56 | |
| FGF-16 | ---MAEVGGVFA | SLDWDLHGFS | SLGNVPL | ADSPGFLMERLGQ | IEGKLQREGSP-- | IDFAH | 55 | |
| FGF-CX | LHGILRRRQLYCRTGFHL | QILPDG | SVQGTQDHSLEGFIS | VAVGLVSI | RGVDSGLYL | | 119 | |
| XFGF-20 | LQSIILRRRQLYCRTGFHL | QILPDG | NVQGTQDHSRFGILEFIS | VA | GLVSI | RGVDGLYL | 116 | |
| FGF-9 | LKGILRRRQLYCRTGFHLE | IFPNGT | IQGTQDHSRFGILEFIS | IAVGLVSI | RGVDSGLYL | | 116 | |
| FGF-16 | LKGILRRRQLYCRTGFHLE | IFPNGT | VHGTQDHSRFGILEFIS | IAVGL | SIRGVDSGLYL | | 115 | |
| FGF-CX | GMNDKGELYGSEKLT | SECI | FREQFEENWYNTYSSNLYKHGDT | GRRYF | VALNKDGT | PRDGA | 179 | |
| XFGF-20 | GMNDKGELYGSEKLT | SECI | FREQFEENWYNTYSSNLYKHGDS | GRRYF | VALNKDGT | PRDGT | 176 | |
| FGF-9 | GMNEKGELYGSEKLT | QECV | FREQFEENWYNTYSSNLYKHVD | GRRYV | VALNKDGT | PRDGT | 176 | |
| FGF-16 | GMNERGELYGSKKLT | REC | VFREQFEENWYNTYASTLYKHS | DSE | QRYF | VALNKDGS | PRDGY | 175 |
| FGF-CX | R | SKRHQKFTTHFLPRP | VDPER | VPPELYKDL | LLMVL | | 211 | |
| XFGF-20 | R | AKRHQKFTTHFLPRP | VDPEK | VPPELYKDL | LMGVS | | 208 | |
| FGF-9 | R | TKRHQKFTTHFLPRP | VDPD | KVPPELYKDL | LSQS | | 208 | |
| FGF-16 | R | TKRHQKFTTHFLPRP | VDPS | KLPMS | SRDL | FHYR | 207 | |

FIGURE 6

pnr:SWISSPROT-ACC:P31371 GLIA-ACTIVATING FACTOR PRECURSOR (GAF) (FIBROBLAST GROWTH FACTOR-9) (FGF-9) (HBGF-9) - HOMO SAPIENS (HUMAN), 208 aa. Identities = 147/208 (70%), Positives = 170/208 (81%)

| | | | | | | | | | | | | | |
|--------|-----|-------|---------|-------|-------|-------|-------|--------|---------|--------|-------|--------|--------------|
| Query: | 1 | MAPLA | EVGGFLG | LEGLG | QQVGS | HFLPP | AGERP | PLLGER | RSAAERS | SARG-G | PGAAQ | LAH | 59 |
| | | | | + | + | + | + | + | + | + | + | + | |
| Sbjct: | 1 | MAPL | GEVGN | YFGVQ | DAV-- | PFGN | VP | LPV-- | DSPV | LLSD | HLGQ | SEAGGL | PRGPA |
| | | | | | | | | | | | | | VDLDH 56 |
| Query: | 60 | LHGIL | RRRL | QLYC | RTG | FHLQ | ILPD | GSVQ | GTRQ | DHSL | FGILE | FISV | AVGL |
| | | | | | | | | | | | | | |
| Sbjct: | 57 | LKGIL | RRRL | QLYC | RTG | FHLQ | ILPD | GSVQ | GTRQ | DHSL | FGILE | FISV | AVGL |
| | | | | | | | | | | | | | |
| | | | | | | | | | | | | | VDSDGLYL 116 |
| Query: | 120 | GMNDK | GELYG | SEKLT | SECIF | REQF | EENW | NTYSS | NIYKH | GD | TGRR | YFVA | LNKDG |
| | | | + | | | | | | | | | | |
| Sbjct: | 117 | GMNEK | GELYG | SEKLT | QECV | REQF | EENW | NTYSS | NIYKH | VD | TGRR | YFVA | LNKDG |
| | | | + | | | | | | | | | | |
| | | | | | | | | | | | | | TPREGT 176 |
| Query: | 180 | RSKR | HQK | FT | TH | FLP | RP | VD | P | ER | V | P | E |
| | | + | | | | | | | | | | | |
| Sbjct: | 177 | RTKR | HQK | FT | TH | FLP | RP | VD | P | ER | V | P | E |
| | | + | | | | | | | | | | | |
| | | | | | | | | | | | | | DKVP |

FIGURE 7

Length = 208

Plus Strand HSPs:

Score = 775 (272.8 bits), Expect = 3.4e-76, P = 3.4e-76
 Identities = 147/208 (70%), Positives = 170/208 (81%), Frame = +1

| | | | |
|--------|-----|--|-----|
| Query: | 1 | MAPLAEVGGFLGGLGQQVGSFHLLPPAGERPPLLGERSSAAERSARG-GPGAAQLAH | 59 |
| Sbjct: | 1 | MAPLGEVGSYFGVQDAV--PFGNVPLPV--DSPVLLNDHLGQSEAGGLPRGPAVTDLDH | 56 |
| Query: | 60 | LHGILRRRQLYCRTGTFHLQILPDGSVQGTQDHSLFGILEFISVAVGLVSIRGVDSGLYL | 119 |
| Sbjct: | 57 | LKGILRRRQLYCRTGTFHLEIFPNGTIQTRKDHRSFGILEFISIAVGLVSIRGVDSGLYL | 116 |
| Query: | 120 | GMNDKGELYGSEKLTSECIFREQFEENWYNTYSSNIYKHGDTGRRYFVALNKDGTPRDGA | 179 |
| Sbjct: | 117 | GMNEKGELYGSEKLTQECVFREQFEENWYNTYSSNLYKHVDTGRRYYVALNKDGTREGT | 176 |
| Query: | 180 | RSKRHQKFTHFLPRPVPDPERVPELYKDIL | 208 |
| Sbjct: | 177 | RTKRHQKFTHFLPRPVPDPDKVPELYKDIL | 205 |

Length = 208

Plus Strand HSPs:

Score = 775 (272.8 bits), Expect = 3.4e-76, P = 3.4e-76
Identities = 147/208 (70%), Positives = 170/208 (81%), Frame = +1

```

Query:
1  MAPLAEVGGFTGGLGLCQQGVGSHFLLPAGERPPLLGERRSAAERSARG-GPGAAQLAH 59
   |||| ||| + | + + | + + || + | || + + | || || |
sbjct: 1  MAPLGEVGSYFGVQDAV--PFGNVPLPV--DSPVLLSDHLGQSEAGGLPRGPVATDLDH 56

Query:
60  LHGILRRRLQYCRGTGFHLQILPDGSVQGTQRQDHSFLFGILEFISVAVGLSVIRGVDGLYL 119
   | ||||| ||||| ||||| + | ++ ||||| + ||||| ||||| |||||
sbjct: 57  LKGILRRRLQYCRGTGFHLEIFPNGTIQGTQRKDHRSRFGILEFISIAVGLSVIRGVDGLYL 116

Query:
120  GMNDKGELYGSEKLTSECIFREQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTPRDGA 179
   ||| + ||||| ||||| || + ||||| ||||| ||||| + ||||| ||||| +
sbjct: 117  GMNEKGELYGSEKLTQECVFRQFEENWNTYSSNLYKHVDTGRRYYVALNKDGTREGT 176

Query:
180  RSKRHQKTFHFLPRPVDPERVPELYKDIL 208
   | + ||||| ||||| ||||| ++ ||||| ||||| +
sbjct: 177  RTKRHQKTFHFLPRPVDPKVPELYKDIL 205

```

FIGURE 9

FGF-CX Query Length = 211
 XFGF-CX Sbjct Length = 208

Plus Strand HSPs:

Score = 906 (318.9 bits), Expect = 4.4e-90, P = 4.4e-90
 Identities = 170/211 (80%), Positives = 189/211 (89%), Frame = +1

| | | | | | | | | | | | | | |
|--------|-----|-------|---------|-------|-------|-------|-------|--------|---------|-------|-------|-------|------|
| Query: | 1 | MAPLA | EVGGFLG | GLEGL | QQVGS | HFLPP | AGERP | PLLGER | SSAAERS | SARGG | PGAAQ | LAHL | 60 |
| | | | + | | | + | | + | | + | | + | + |
| Sbjct: | 1 | MAPL | ADVGT | FLGGY | DALGQ | -VGS | HFLPP | AKDSPL | LFNDP | LAQSE | RLSR | SAP-- | 57 |
| | | | | | | + | | | | | | | 120 |
| Query: | 61 | HGIL | RRRL | QLYC | RTGF | HLQIL | PDGS | VQGT | RQDHS | LFGIL | EFIS | VAVGL | VSIR |
| | | | | | | | | | | | | | 117 |
| Sbjct: | 58 | QGIL | RRRL | QLYC | RTGF | HLQIL | PDGN | VQGT | RQDHS | RFGIL | EFIS | VAVGL | VSIR |
| | | | | | | | | | | | | | 180 |
| Query: | 121 | MNDK | GELY | GSEK | LITSE | CI | FR | EQFE | ENWY | NTYSS | NIYKH | GDTG | RRYF |
| | | | | | | | | | | | | | 177 |
| Sbjct: | 118 | MNDK | GELF | GSEK | LITSE | CI | FR | EQFE | ENWY | NTYSS | NIYKH | GDSG | RRYF |
| | | | | | | | | | | | | | 211 |
| Query: | 181 | SKRH | QKFT | HTFL | PRP | VDPE | RVPE | LYK | DLL | MYT | 211 | | |
| | | | | | | | | | | | | | 208 |
| Sbjct: | 178 | AKRH | QKFT | HTFL | PRP | VDPE | KVPE | LYK | DLM | GYS | 208 | | |

FIGURE 10

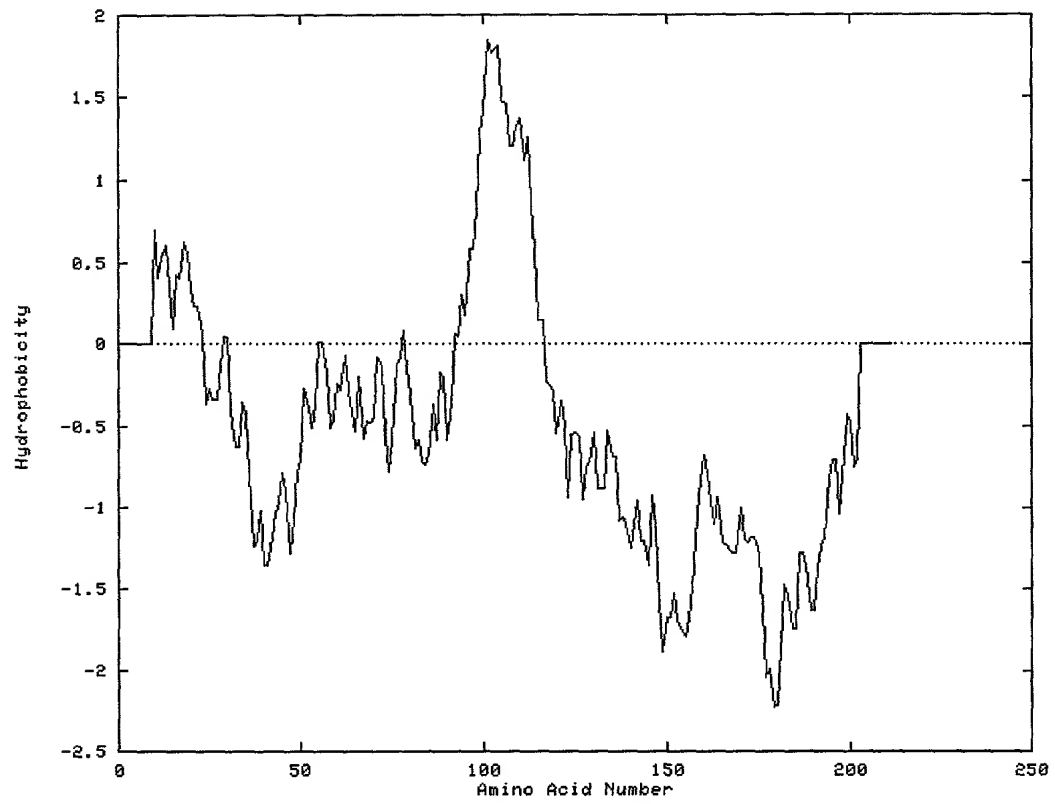


FIGURE 11

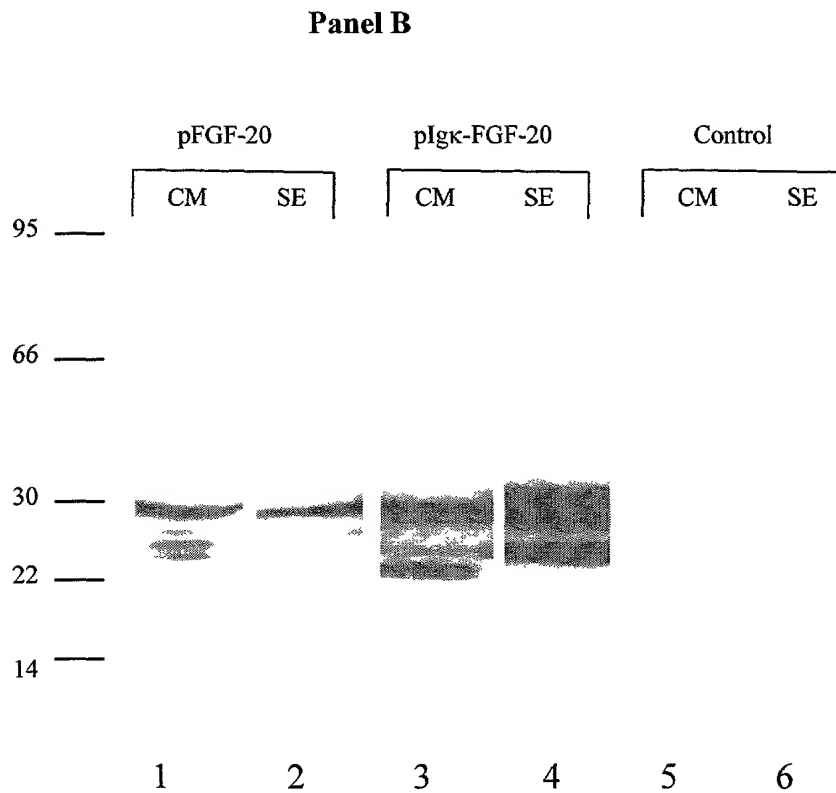
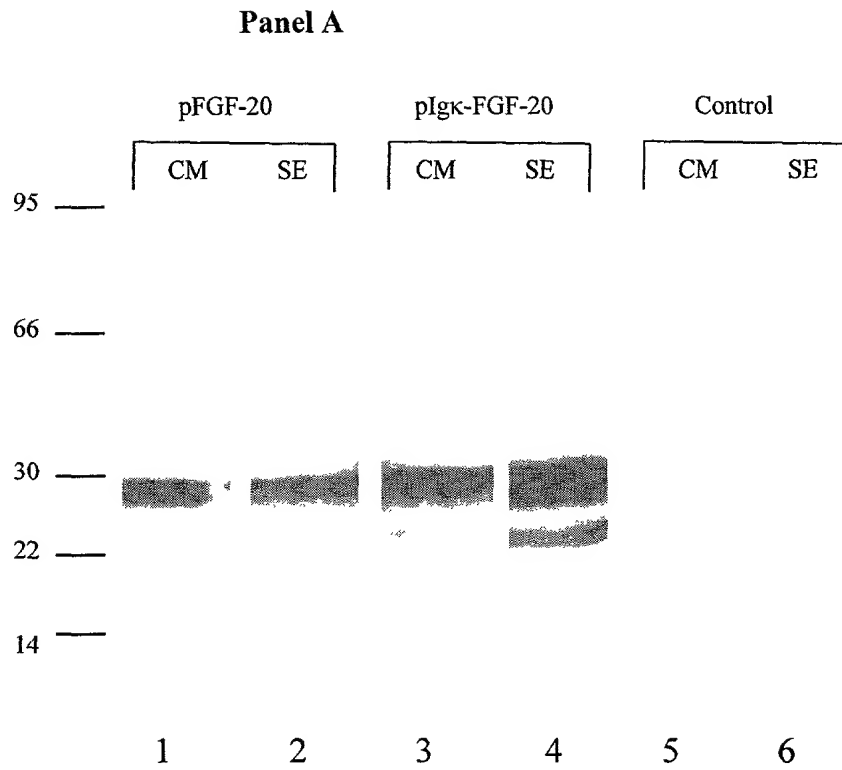


FIGURE 12.

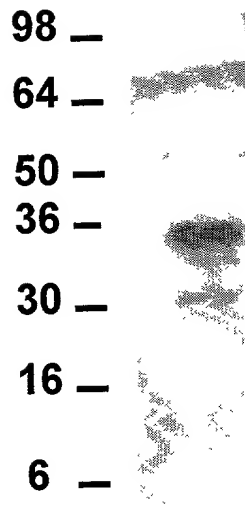


Figure 13.

Exon 1
...AGACAGTGAGAGCTTCCCTGCCATTTCAGTGCAAAGTCCCTCCGGAGCGACCTCAGAGGAGTAACCGGCGCTTAACT
TTTTGCGCTCGTTTIGCTATAATTTTCTCTATCCACCTCCACCCCCACAACACTCTTTACTGGGGGGTCTTTT
GTGTTCCGGATCTCCCCCTCCATGGCTCCCTTAGCCGAAGTCGGGGGCTTTCTGGGGCGCCTGGAGGGCTTGGGCCAGCA
M A P L A E V G G F L G G L E G L G Q Q
1 GGTGGTTTCGCAATTCCTGTTCCTCCTGCCGGGAGCGCGCGCTGCTGGCGAGCGCAGGAGCGGGCGGAGCGGA
21 V G S H F L L P P A G E R P P L L G E R R S A A E R S
CGCGCGCGGGGGGGCTGCGCAGCTGCGCACCTGCGCATCCTGCGCGCGGAGCTCTATTGCCGCACC
48 A R G G P G A A Q L A H L H G I L R R R Q L Y C R T
<-|-> **Exon 2**
GGTTCCACCTGCAGATCCTGCCCGACCGGAGCGGTGCAGGGCACCCGGCAGGACCCACAGCCTCTTCGGTATCTTGGAAAT
74 G F H L Q I L P D G S V Q G T R Q D H S L F G I L E F
CATCAGTGTGGCAGTGGGACTGGTCAGTATTAGAGGTGTGGACAGTGGTCTCTATCTTGGATGAATGACAAAGGAGAAC
101 I S V A V G L V S I R G V D S G L Y L G M N D K G E L
<-|-> **Exon 3**
TCTATGGATCAGAGAAACTTACTTCCGAATGCATCTTTAGGGAGCAGTTTGAAGAGAACTGGTATAACACCTATTCTATCT
128 Y G S E K L T S E C I F R E Q F E E N W Y N T Y S S
AACATATATAACATGGAGACACTGGCCGAGGTATTTGTGGCACTTAACAAAGACGGAACCTCCAAGAGATGGCGCCAG
154 N I Y K H G D T G R R Y F V A L N K D G T P R D G A R
GTCCAAGAGGCATCAGAAATTTACACATTTCTTACCTAGACCAGTGGATCCAGAAAGAGTTCCAGAATTGTACAAGACC
181 S K R H Q K F T H F L P R P V D P E R V P E L Y K D L
TACTGATGTACACT**TGA**...
208 L M Y T

Figure 14.

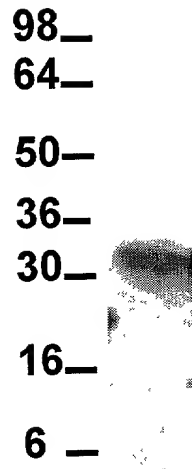


Figure 15, Panel A.

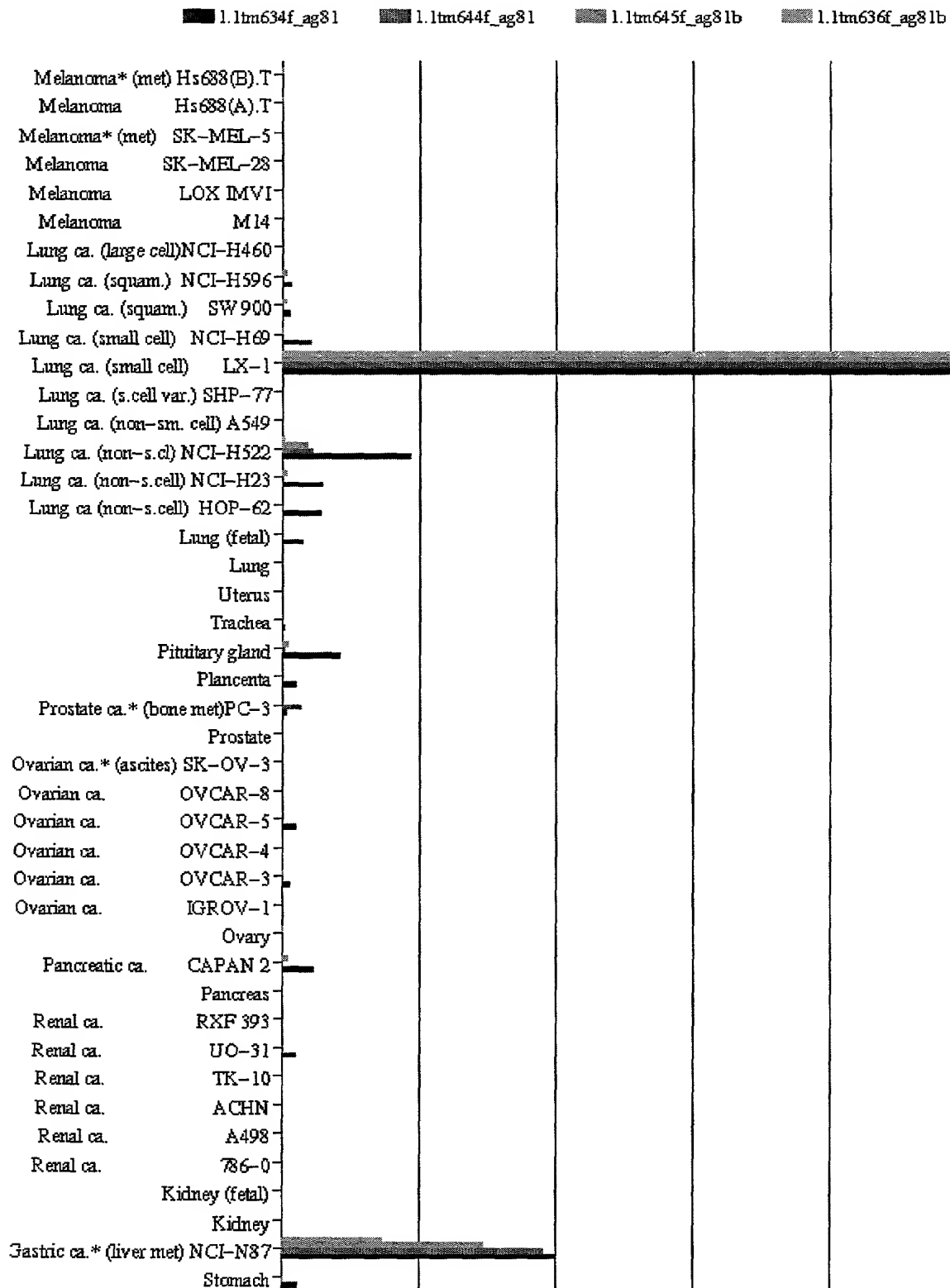


Figure 15, Panel B.

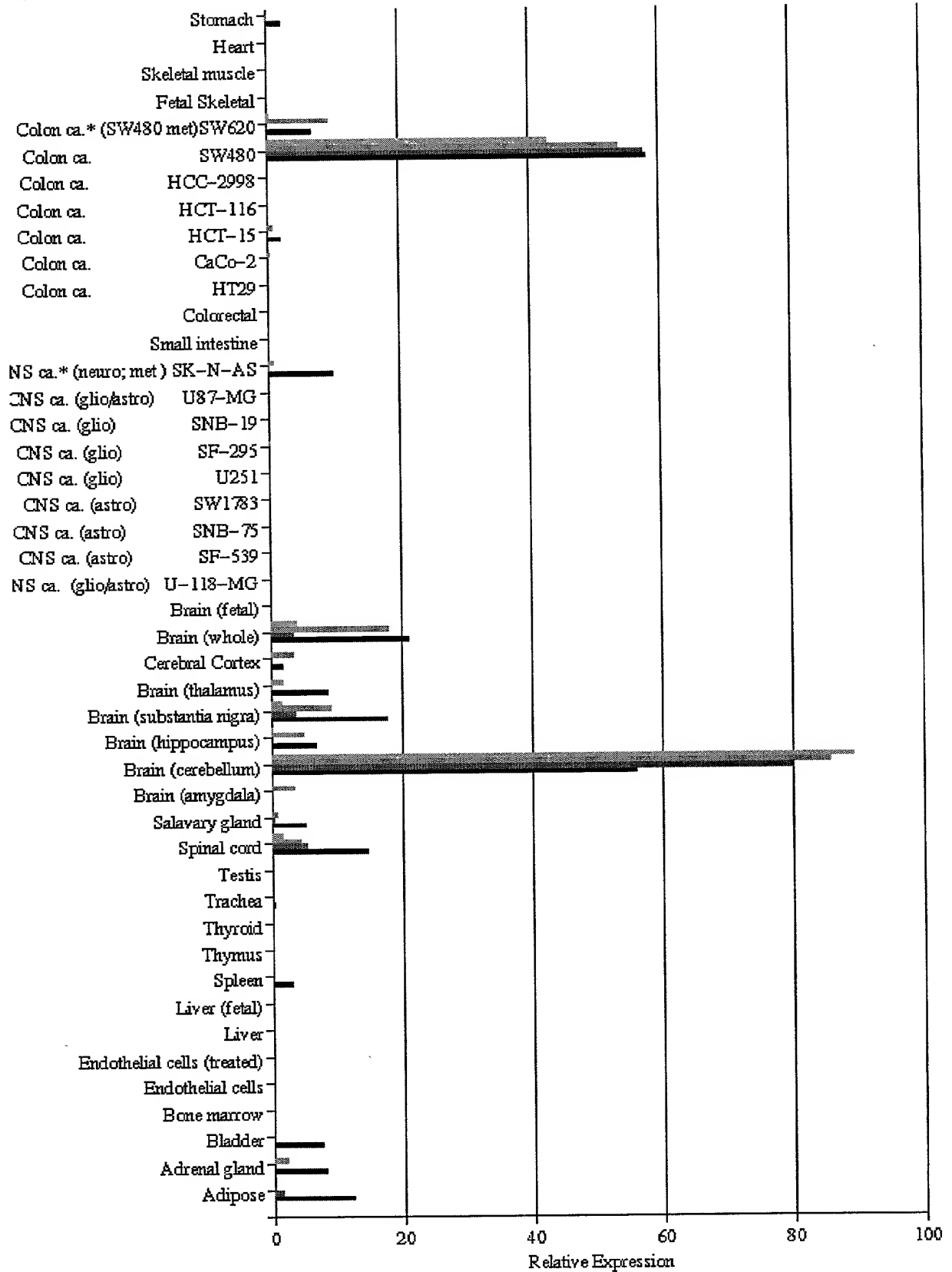


Figure 15, Panel C.

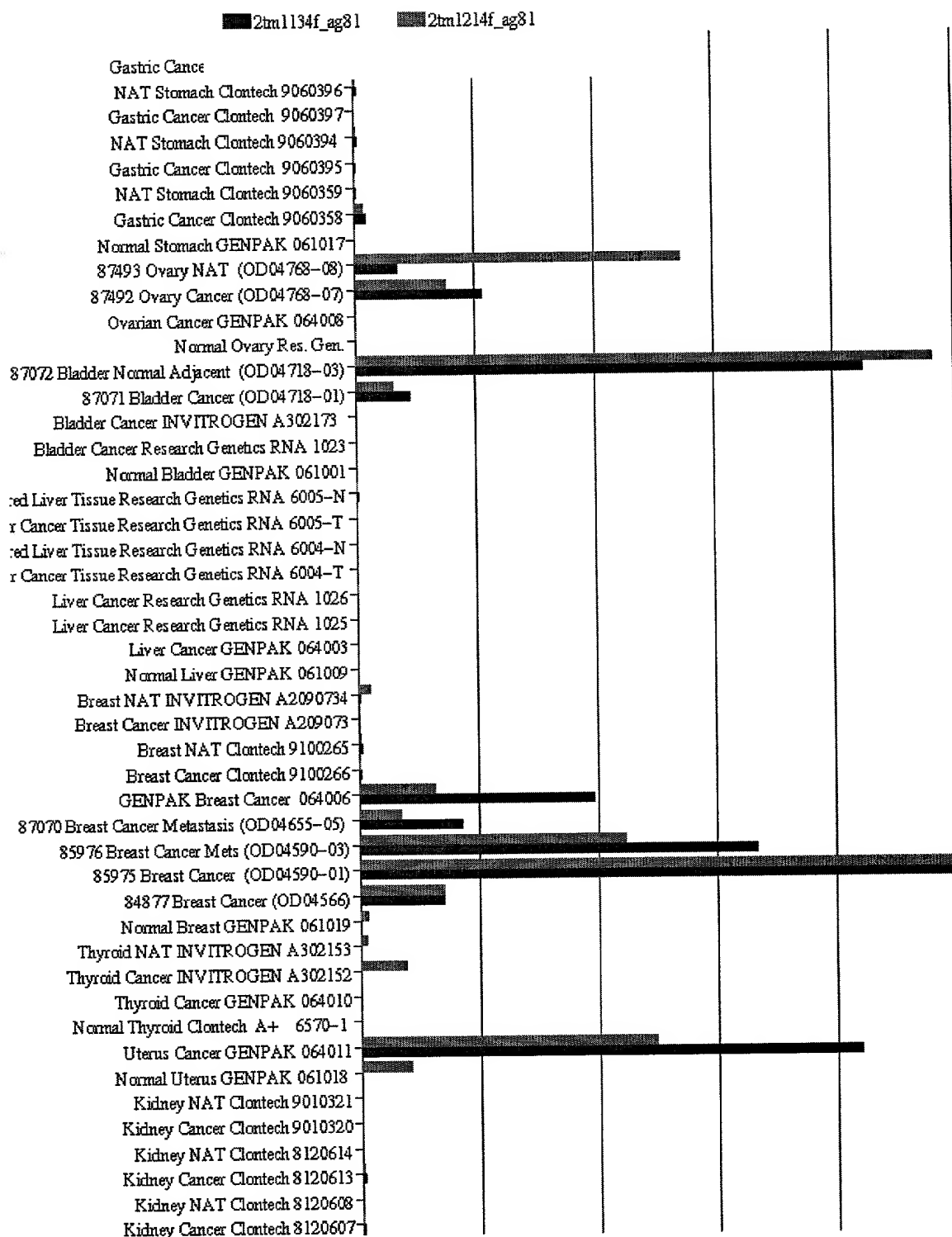


Figure 15, Panel D.

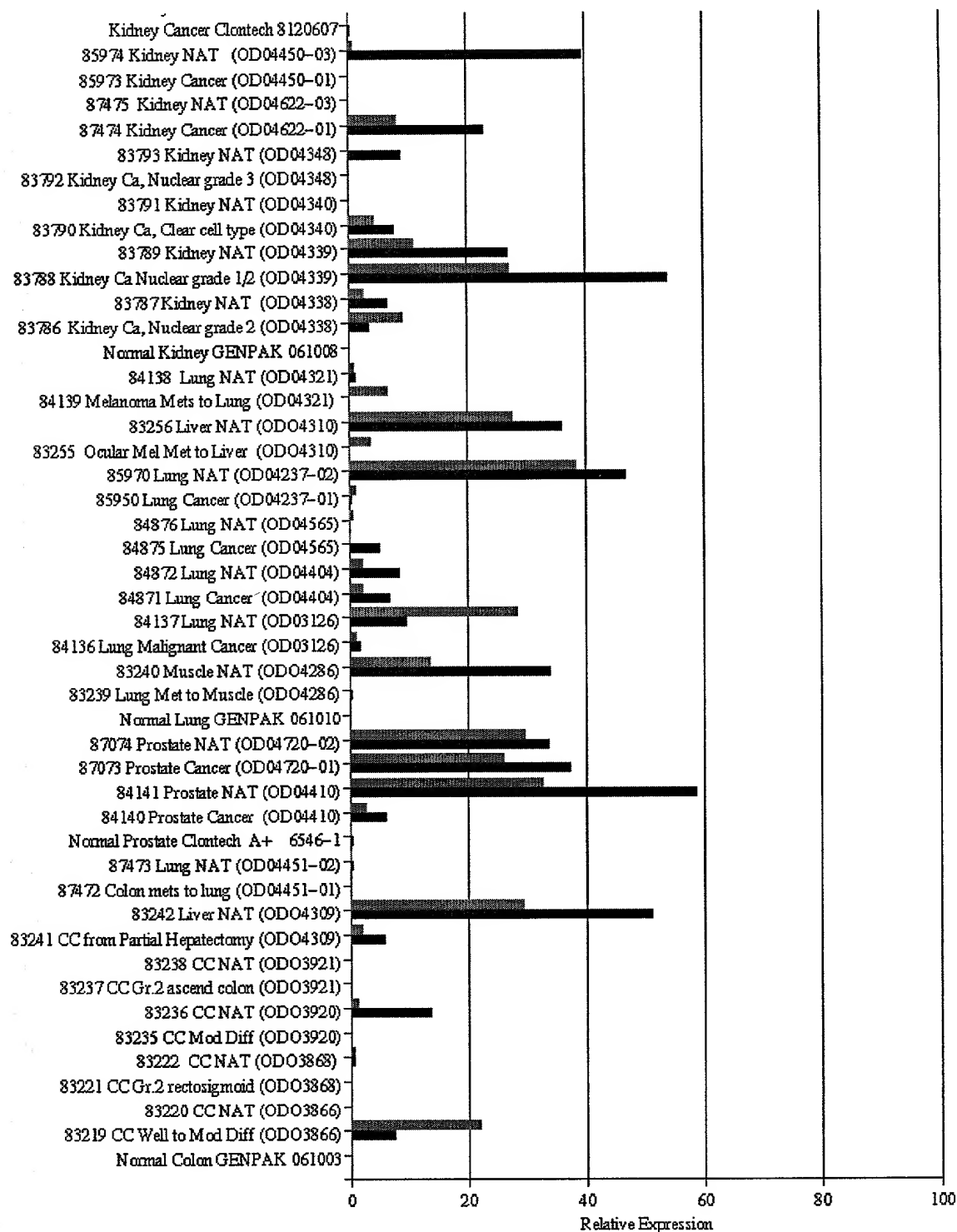


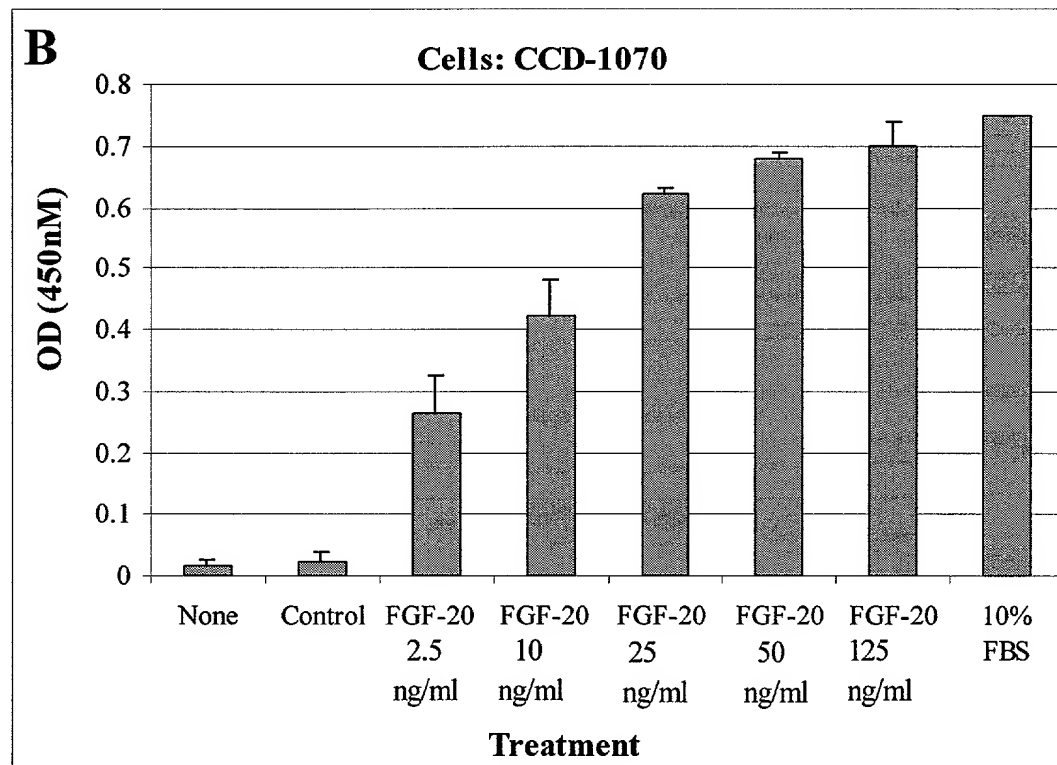
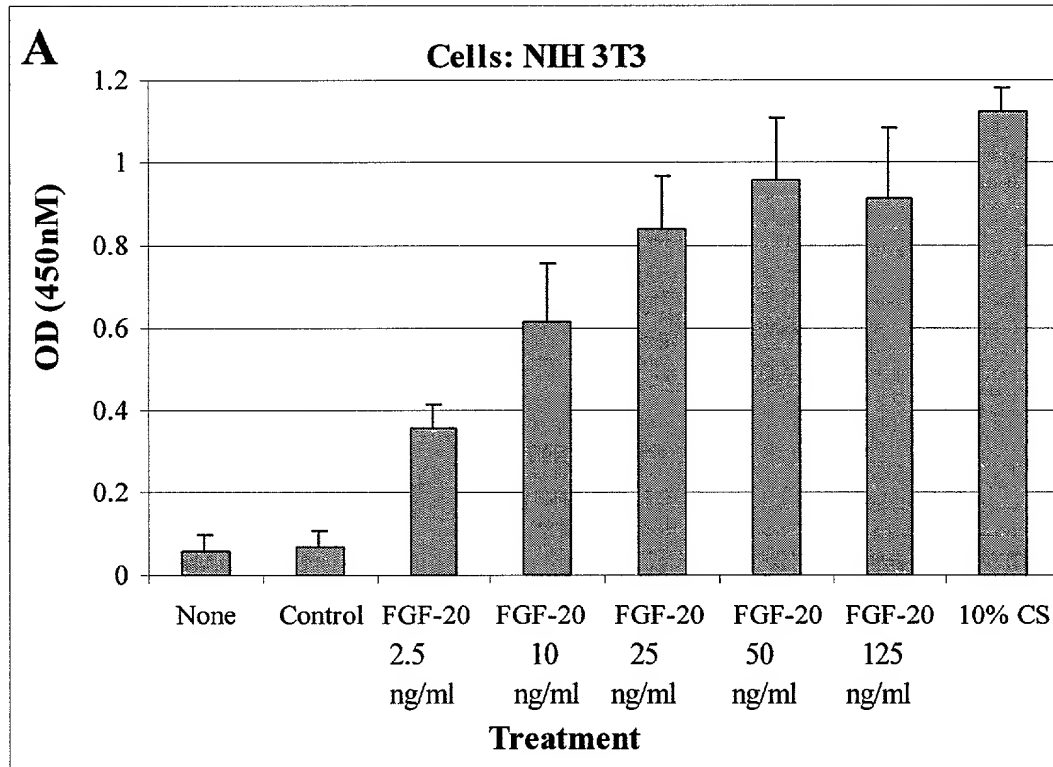
FIGURE 16.

FIGURE 16 (continued).

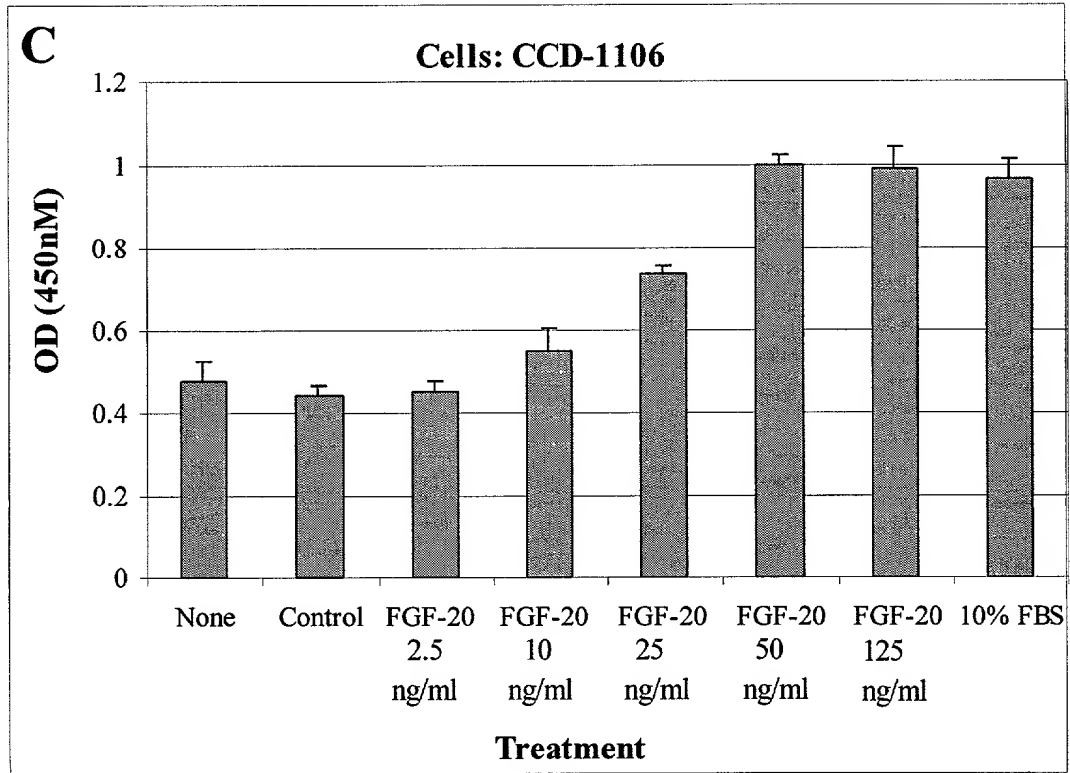


FIGURE 17.

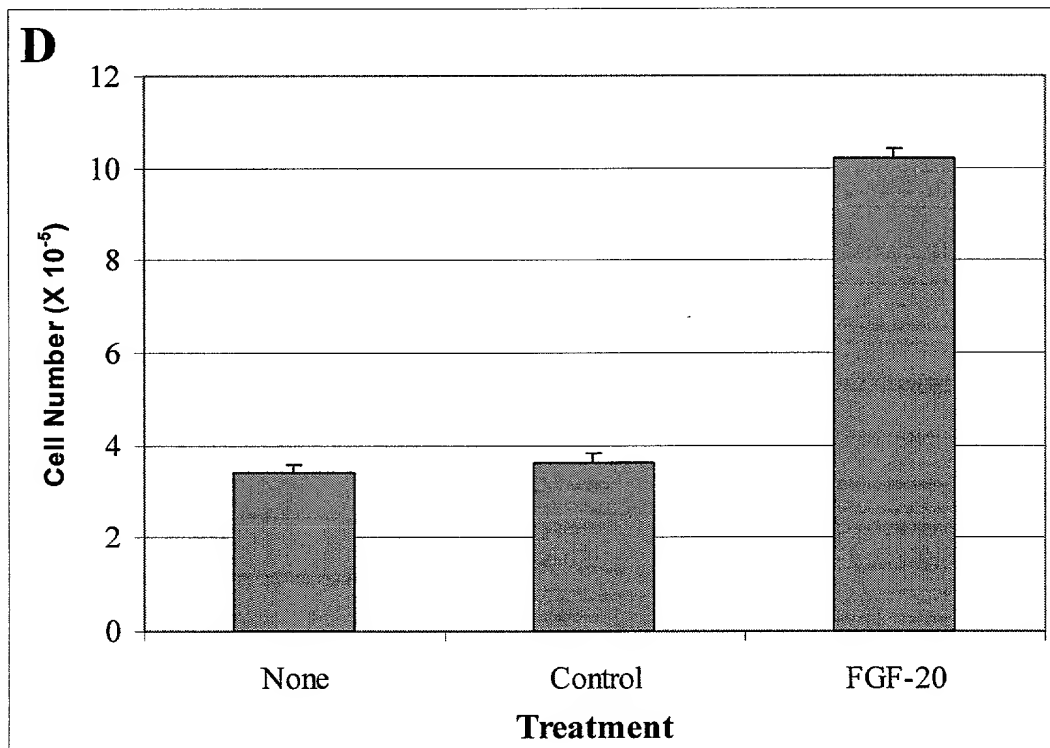


FIGURE 18.

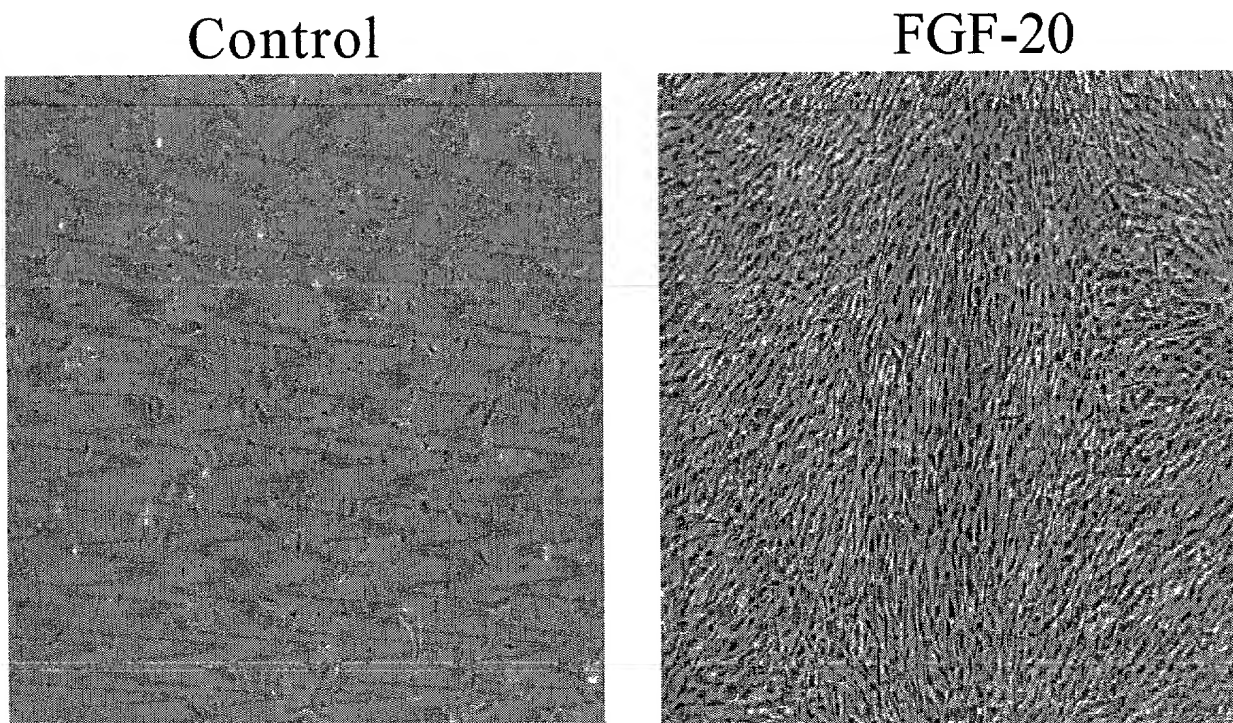


FIGURE 19.

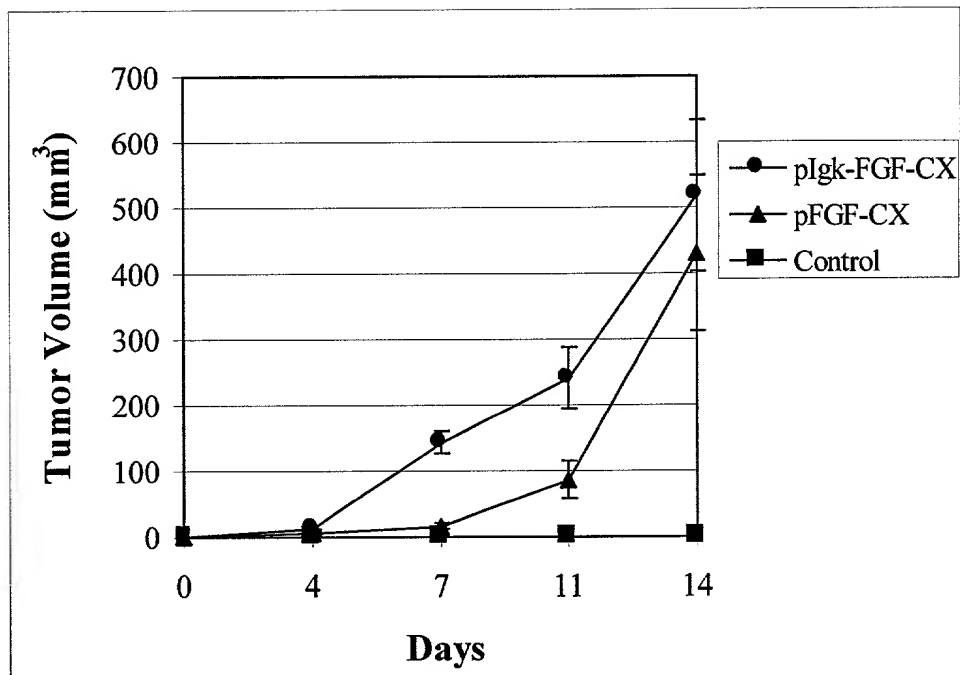
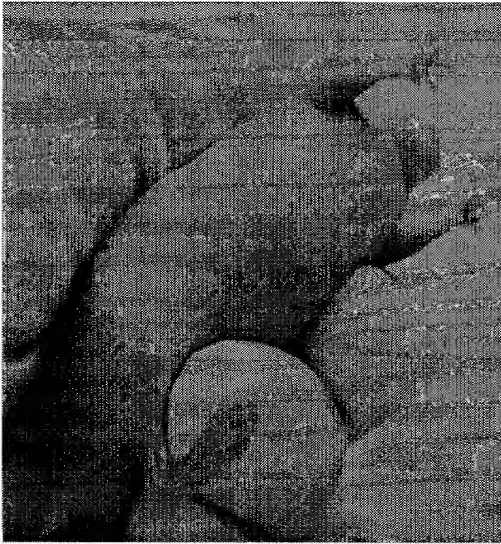


FIGURE 20.

Control



CG-AB020858

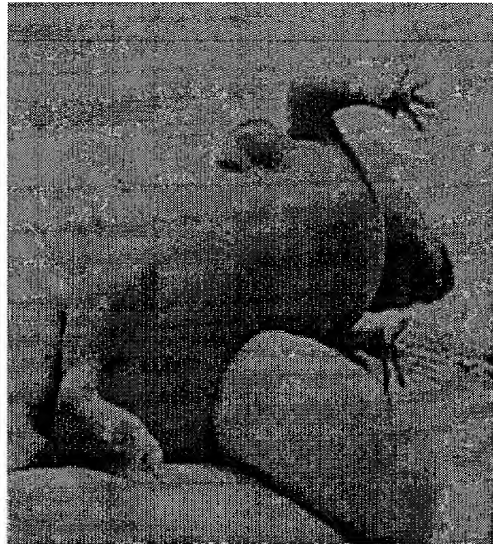


FIGURE 21.

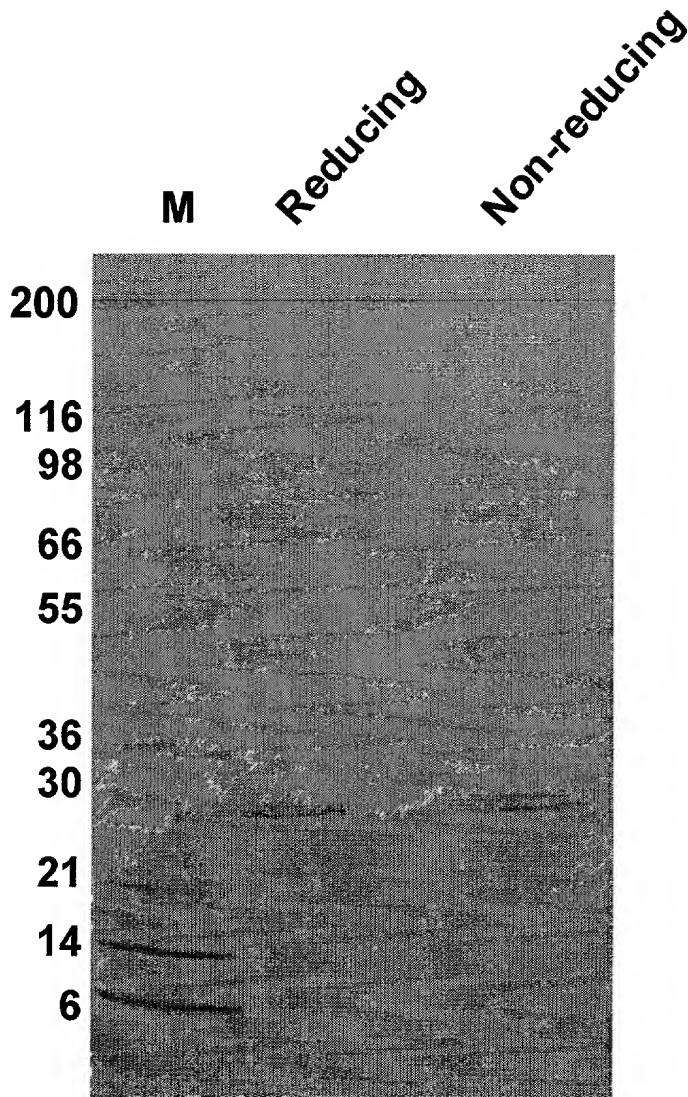


FIGURE 22.

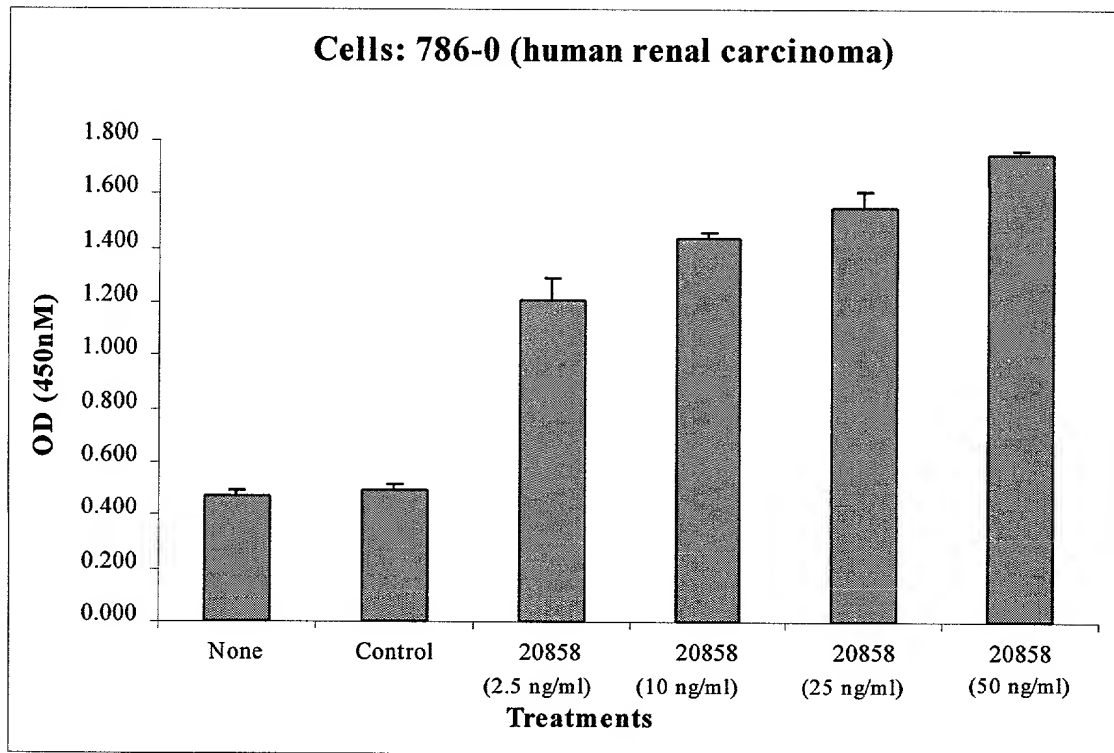
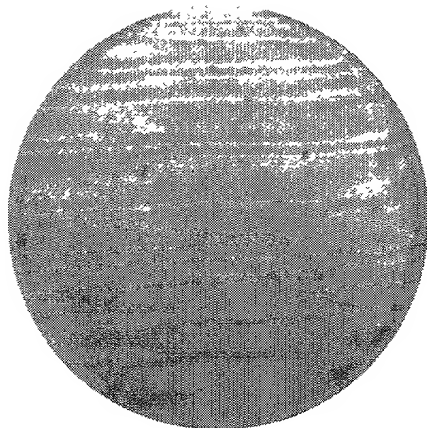


FIGURE 23.

Control



pFGF-20



pIgk-FGF-20

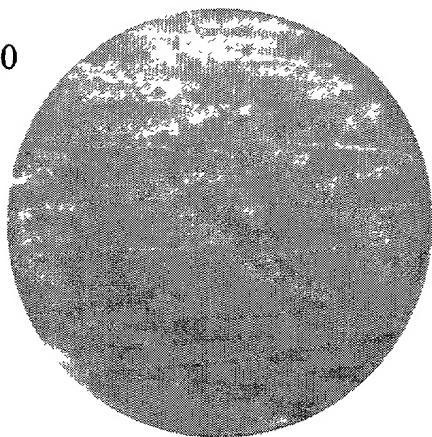


FIGURE 24

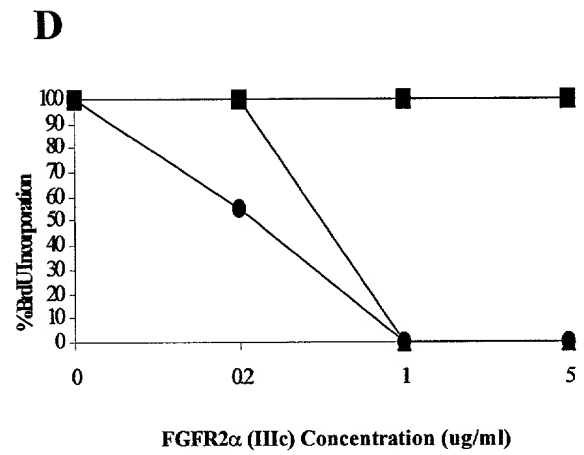
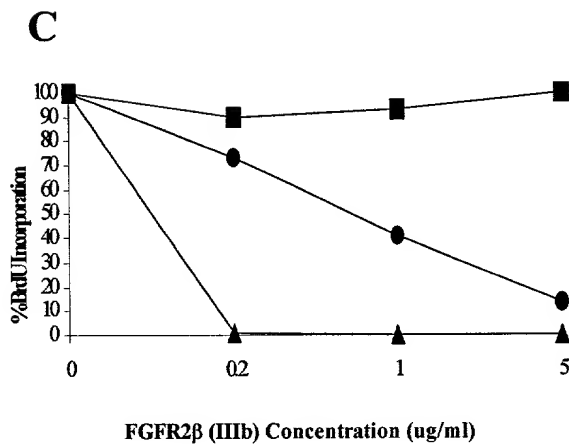
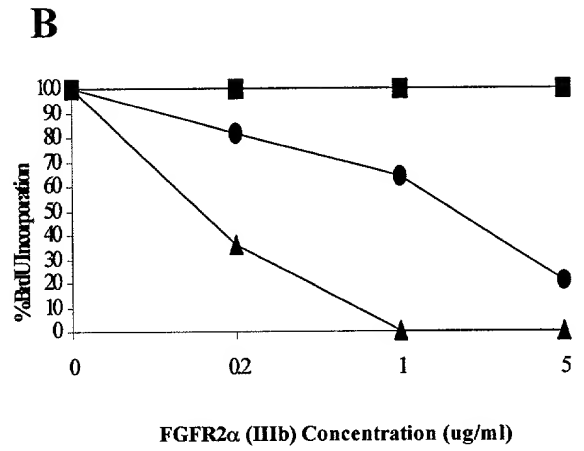
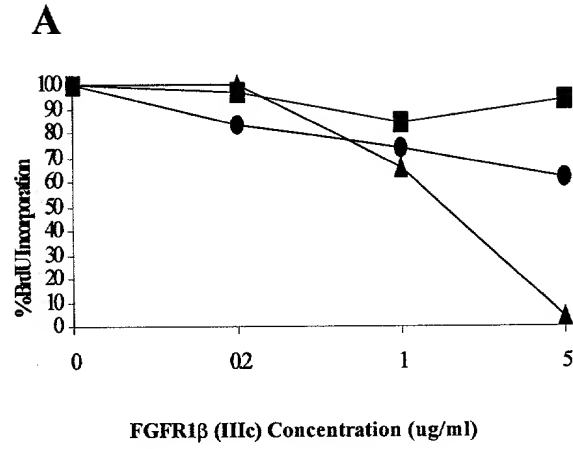


FIGURE 24 (ctd)

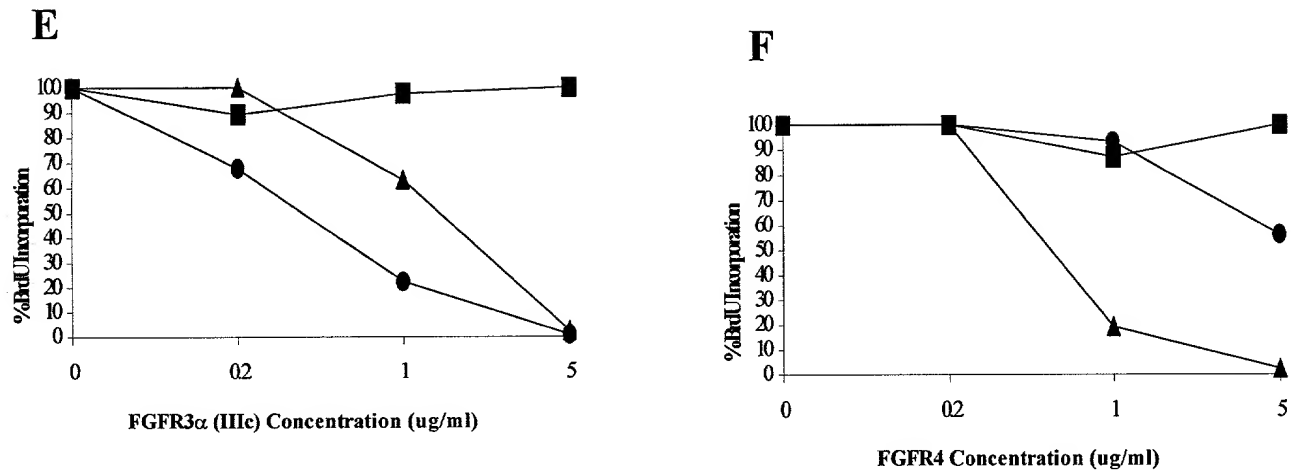


FIGURE 25

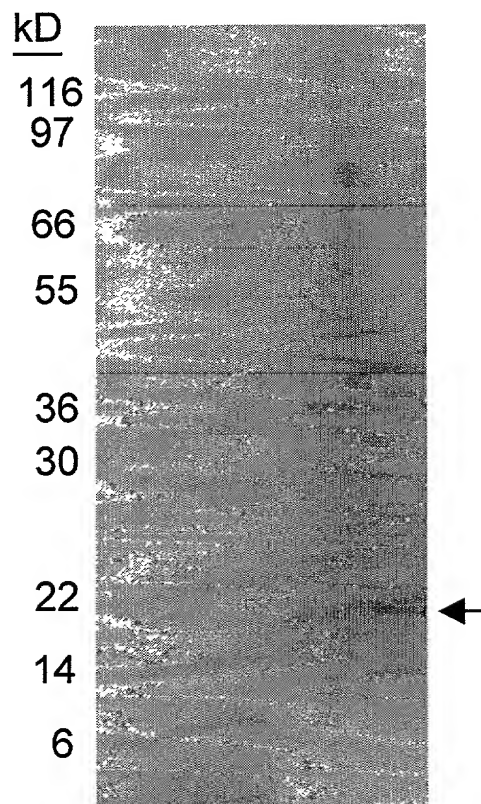


FIGURE 26

